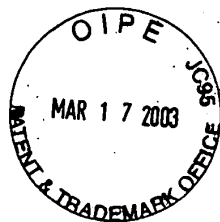SEQUENCE LISTING

(1) GENERAL INFORMATION:

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        (C) CITY: Oxford

        (E) COUNTRY: United Kingdom

        (F) POSTAL CODE (ZIP): OX3 9QH

    (ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS

    (iii) NUMBER OF SEQUENCES: 39

    (iv) COMPUTER READABLE FORM:

        (A) MEDIUM TYPE: Floppy disk

        (B) COMPUTER: IBM PC compatible

        (C) OPERATING SYSTEM: PC-DOS/MS-DOS

        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

    (A) APPLICATION NUMBER: WO PCT/GB96/01341

    (B) FILING DATE:05-JUN-1996

(vi) PRIOR APPLICATION DATA:

    (A) APPLICATION NUMBER: GB 9511439.3

    (B) FILING DATE:06-JUN-1995

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    (A) NAME: Warren M Cheek, Jr.

    (B) REGISTRATION NUMBER: 33,367

    (C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US

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    (B) TELEFAX: (202)-721-8250

    (C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 723 base pairs

        (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
CCCGGTCGGA GGTTTCAAGG AATGACTAGA TGTGGCACTT AGTGCCATGG TCTAGTTGAC        60

AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTCAG AGTTTTTTTC CAGCCTTAAT       120

AATTCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTTGA GCGAAGTTTG TTTGGGGATT       180

TTAGTTTGGT TTCCCTGTCA CTGTTTTCTT TCCTTGAAAC TGACTTTCAT TTGCAACATG       240

AGAATTGCTG TATTTGTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA       300

CATTTAGGGA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTTGGG       360

ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC       420

ATTAATTGCT TGTTTTATGA AACCACTCTT TTTTTTTTTT TTTTTTTTTT GGCTTCTTCA       480

TATCCTGTGG TAATGAGTTA ATGCATTTAG AAGCACATGG CAGAACTAGG AGATCTGTGG       540

ATGACAGTGG TACAGGAGCT CTGAATTTTT TAGATAAACT ATGAGAGTGG AAACAGAAAT       600

CTGAGGCTAG TTTCTTGAGC TGACTGTAAA TTTTGTGAGA ATATTTTCAA GACTACATTA       660

GTTGTGTGTT TGAGGAAAAA TAAAATGTTT AAGTTGTCCA TTCCTTGAAA CCTCCCGACC       720

GGG                                                                      723
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATTCTTCCAG ATGATCCTGA TAAAAAACCA CAAGCAAAAC AGTTACAGAC CAAAAAACCA   60

CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT   120

GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG   153

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:

       (A) LENGTH: 153 base pairs

       (B) TYPE: nucleic acid

       (C) STRANDEDNESS: double

       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC   60

CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA AATTACTGAA TAAAGACCTT   120

GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA   153

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:

       (A) LENGTH: 153 base pairs

       (B) TYPE: nucleic acid

       (C) STRANDEDNESS: double

       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC CAAGAAACCC   60

CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT   120

GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA   153

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 153 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA   60

CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT   120

GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA   153

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 41 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

    Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln

```
1                    5                    10                    15
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Ser Arg Asp Leu Ala Lys
              20                    25                    30
Arg Glu Ala Gln Arg Leu Cys Gly Ala
         35                    40
```

(2) INFORMATION FOR SEQ ID NO: 7:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 41 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
1                    5                    10                    15
Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
              20                    25                    30
Lys Glu Ala Gln Arg Leu Ala Gly Ala
         35                    40
```

(2) INFORMATION FOR SEQ ID NO: 8:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 41 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

    Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
    1   5   10   15

    Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
                20   25   30

    Lys Glu Ala Gln Arg Leu Ala Gly Ala
            35   40

(2) INFORMATION FOR SEQ ID NO: 9:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 41 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

    Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln
    1   5   10   15

    Thr Arg Ala Asp Tyr Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg
                20   25   30

    Lys Glu Val Gln Arg Leu Thr Gly Ala
            35   40

(2) INFORMATION FOR SEQ ID NO: 10:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 6608 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG AAGGCCTGGC        60

CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG       120

CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAG AAAGGGGATT CTTGACCTAC       180

ACCTTGTAAC CTGAGTGGAC TTTCTTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA       240

GTGATGAAGA AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG       300

GGTCAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA       360

GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG       420

AGTCTGACAC ATCTAGAGAG AAGAAACAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT       480

CTGAGTTTTG GAAGTCCAGT CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA       540

AGCAACAGCA ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA       600

GTAGTGAAGA TTCTGCCGAT GATTCGTCCA GTGAAACTAA GAAGAAAAAG CATAAAGATG       660

AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGGTTCTGAT TCTGAATCGG       720

CGGAAGATGG GGATAAAAGC AGTTGTGAAG AAAGTGAATC TGACTATGAG CCAAAAAACA       780

AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG       840

GACAGAAGAA GAGGCAACTT GATTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG       900

ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA       960

CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCA CAGACTGAAG      1020
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AAGATGAATT TGAAACTATA GAGAAGTTTA TGGACAGTCG AATTGGCCGA AAAGGAGCCA   1080

CTGGTGCCTC AACCACCATC TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTTG   1140

AAAAGTCAAA GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA   1200

TCCATAACAC TTGGGAAACT GAAGAAACGC TGAAGCAACA AAATGTTAAA GGAATGAACA   1260

AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG CTGGCTGAAA AATGCTTCTC   1320

CAGAAGATGT GGAATATTAT AACTGCCAGC AGGAGCTTAC AGATGATCTG CACAAACAAT   1380

ATCAAATAGT GGAAAGAATA ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTTATCCGG   1440

ACTACTATTG CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGGAA GATGGTGCTC   1500

TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATTT TAGCAGAAAT CAATCCAAGA   1560

CTACTCCCTT TAAGGACTGC AAGGTTCTAA AACAGAGACC AAGATTTGTT GCACTGAAGA   1620

AGCAACCATC TTACATTGGA GGACATGAAA GTCTGGAGTT AAGAGATTAT CAGTTAAATG   1680

GATTGAATTG GCTCGCTCAT TCATGGTGCA AAGGAAATAG TTGTATTCTT GCAGATGAAA   1740

TGGGTCTGGG TAAAACAATA CAAACAATTT CTTTTCTGAA CTACCTGTTT CATGAACATC   1800

AACTGTATGG CCCTTTTCTT CTGCGCGTGC CACTTTCTAC CTTGACATCT TGGCAAAGAG   1860

AGATTCAAAC TTGGGCTCCT CAGATGAATG CTGTAGTTTA CTTAGGAGAT ATAACTAGTA   1920

GAAATATGAT AAGGACTCAT GAATGGATGC ATCCACAGAC TAAACGATTA AAGTTTAACA   1980

TACTTCTGAC GACATATGAA ATTTTACTGA AGGATAAGTC ATTCCTTGGT GGTCTCAATT   2040

GGGCATTCAT AGGAGTTGAT GAAGCTCATC GTTTAAAAAA TGATGACTCT CTTCTGTACA   2100

GGACTTTAAT AGACTTTAAG TCCAACCATC GACTTCTGAT TACTGGAACC CCACTGCAAA   2160

ATTCCCTCAA AGAGCTGTGG TCTTTGTTGC ATTTCATCAT GCCAGAAAAA TTTTCCTCCT   2220

GGGAAGATTT TGAAGAGGAG CATGGCAAAG GAAGAGAGTA TGGTTATGCA AGTCTTCACA   2280

AAGAGCTTGA ACCATTTTTA CTAAGAAGAG TTAAAAAAGA TGTAGAAAAG TCTTTACCTG   2340

CTAAGGTTGA ACAAATTCTG AGGATGGAAA TGAGTGCATT GCAGAAGCAA TATTACAAGT   2400

GGATTTTAAC AAGGAATTAT AAAGCCCTCA GTAAAGGTTC AAAAGGCAGT ACCTCAGGCT   2460

TTCTGAACAT TATGATGGAA CTTAAGAAGT GTTGTAACCA TTGCTACCTC ATTAAGCCAC   2520

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CAGATGATAA TGAATTCTAT AATAAACAGG AGGCCTTACA GCATTTGATA CGTAGCAGCG    2580

GGAAACTAAT CCTTCTTGAC AAGCTACTGA TTCGTCTGCG AGAACGTGGC AACAGAGTTC    2640

TGATTTTCTC TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATCGCC    2700

AGTTTCCCTT CCAGAGACTT GATGGATCAA TAAAAGGGGA ATTGAGGAAG CAAGCACTGG    2760

ATCATTTCAA TGCAGAAGGA TCAGAGGATT TCTGTTTTTT ACTGTCTACA AGAGCTGGAG    2820

GATTAGGTAT TAACTTGGCA TCTGCTGACA CTGTAGTTAT TTTTGATTCT GACTGGAATC    2880

CACAGAATGA TCTGCAGGCA CAGGCGAGAG CTCATAGAAT TGGACAGAAG AAACAGGTTA    2940

ATATTTATCG GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA    3000

AGAAGATGGT GCTAGACCAT TTAGTAATTC AGAGAATGGA CACGACAGGA AAAACTGTTC    3060

TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTTAA TAAAGAAGAG TTATCAGCTA    3120

TTTTGAAGTT TGGTGCTGAG GAACTCTTTA AAGAACCTGA AGGAGAAGAA CAGGAGCCCC    3180

AGGAAATGGA TATAGATGAA ATCTTGAAGA GAGCTGAAAC TCGGGAAAAT GAGCCAGGTC    3240

CATTGACTGT AGGGGATGAG TTGCTTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG    3300

ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAATTGGGAA GAAATCATCC    3360

CAGAATCCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA AAAAGAACTT GAAGAAATAT    3420

ACATGCTCCC GAGGATGAGA AACTGTGCAA AACAGATCAG CTTTAATGGG AGTGAAGGAA    3480

GACGCAGTAG GAGCAGAAGA TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC    3540

GGCCAAAAAA GCGTGGAAGA CCTCGAACCA TTCCTCGAGA AAATATTAAA GGATTTAGTG    3600

ATGCAGAGAT CAGGCGGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT CTGGAAAGGT    3660

TAGATGCTGT AGCTAGAGAT GCTGAACTGG TTGATAAATC TGAGACAGAC CTTAGACGTT    3720

TGGGTGAACT TGTACATAAT GGATGCATTA AGGCTTTAAA GGACAATTCA TCTGGACAAG    3780

AAAGAGCAGG AGGTAGACTT GGGAAAGTTA AAGGCCCAAC GTTTCGAATC TCAGGAGTGC    3840

AGGTGAATGC AAAACTAGTC ATCTCTCACG AAGAAGAGCT GGCACCACTG CACAAATCCA    3900

TTCCTTCAGA TCCAGAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC AAGGCTGCTC    3960

ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT GTTAGTAGGC ATCTATGAAT    4020
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ATGGCTATGG CAGCTGGGAA ATGATAAAAA TGGATCCAGA TCTCAGCTTA ACACAGAAGA    4080

TTTTACCTGA TGATCCAGAC AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT    4140

ACCTCATTAA ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAAGG CTTGCTGGTG    4200

CAGGCAATTC CAAGAGAAGG AAGACAAGAA ATAAGAAGAA TAAGATGAAG GCTTCAAAAA    4260

TAAAAGAAGA AATAAAGAGT GATTCTTCAC CACAACCCTC AGAAAAATCT GATGAAGATG    4320

ATGAGGAGGA GGATAACAAG GTAAATGAAA TGAAATCTGA AAATAAGAA AAATCTAAAA    4380

AAATTCCATT GCTGGATACT CCAGTTCATA TTACTGCAAC CAGTGAACCA GTTCCTATCT    4440

CAGAAGAATC TGAAGAACTC CATCAGAAGA CATTTAGTGT GTGCAAAGAA AGAATGAGGC    4500

CTGTCAAAGC AGCACTGAAA CAGCTGGATA GACCAGAGAA GGGCCTTTCT GAAAGGGAGC    4560

AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGGA TCACATTACA GAATGCCTGA    4620

AGGAGTACAC AAATCCCGAG CAAATAAAAC AGTGGAGGAA AAATTTGTGG ATTTTTGTGT    4680

CCAAGTTTAC AGAATTTGAT GCCAGAAAGC TGCACAAACT CTACAAACAT GCAATCAAAA    4740

AGCGCCAAGA GTCTCAGCAA CACAATGACC AAAACATTAG CAGCAATGTG AATACACATG    4800

TAATCAGAAA TCCAGATGTG GAAAGACTGA AGGAGACTAC AAACCATGAT GATAGTAGCA    4860

GGGACAGTTA TTCTTCTGAT AGACATTTAT CACAATACCA TGATCATCAC AAAGACAGGC    4920

ATCAGGGAGA TGCTTACAAG AAAAGTGACT CCAGGAAAAG GCCATATTCA GCCTTCAGTA    4980

ATGGAAAAGA TCACAGAGAC TGGGATCACT ACAAACAGGA CAGCAGATAC TACAGTGATA    5040

GTAAACATAG AAAGTTAGAT GACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA    5100

ACTTAAAAGA CAGCCGGGGT CATTCAGATC ACCGCTCCCA TTCAGACCAC AGGATACACT    5160

CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAATC TTCGAGAGAT TATAGATACC    5220

ACTCAGACTG GCAAATGGAC CACAGAGCTT CTGGTAGTGG CCCGAGGTCA CCACTAGATC    5280

AGAGGTCTCC TTATGGTTCA AGATCTCCCC TAGGACACAG ATCTCCATTT GAACACTCAT    5340

CAGATCACAA AAGTACACCT GAACATACAT GGAGTAGCCG GAAGACATAA CAAAGACTGA    5400

CATTTTCTGG ACCTTCTTTT TAGCCATATA CAGTAAACTA ACACAGTAAT TGCCTTACAT    5460

GACTTGAAAG ATATGGACTG GATATTCTAT CAGTAGCAGT ATTGTTACTT CTTTCCAGGA    5520
```

```
TGCAAGGTCT ATTATCCCAA CAGAAGAAAA ATATTTTTGT ATTTAAAGTT TATGCTGCAC    5580

TGTGCTGCAA ATGTTGTGGC ACTTTTTTTT TAAGAAATGG AAGATGTTTA CTTTTACAGG    5640

GACCTCAACA CTGCCCCTTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG    5700

TTCTAGGCTG AACACAGATT AAATTATGTT TGTAAATGAA CACTTAAACA CTGACCTGTG    5760

CTTATGTTTC AGGAAGAAT GGGGGATTTA TTTTGTTTTA TTTCTTGGTA GAGAACTCTC    5820

AAGGACTTTG TTCACTTTCC AAAGCTACTT GTTACATTG TACACTGCGA CCACCTTGCC    5880

GCTTTTCATC ACAAGCTTGA ATATTTAAAT TCTGTACCTA CAGTTGTAAA ATAGCCAGGA    5940

TTTCTCCTGT TTGTGATCAG TTATAATGCC TTTTTATGAA ACAAACAAAC AAACAAAAAA    6000

CAATTAAAAA AAAAAACACA ACAAAACCAA CAAATGGCTG TAAATTATTG TAAATTAATT    6060

AAATGAGCTT TTTTCCGTCA GGCTTTTTTT GGCTGTTCCT TTCCCCAACA ACTCAGGCCT    6120

TCTTTTCACA AAGTCAGTAT ACTTACATGT TTTAATAAAA TATCTCGATG GAATCAGAAT    6180

GTAAAAATGG GGAAGGGAAT ATTTTATTCC ATTTAGTGCT CCTTTTTTAT TGGATACTTT    6240

TACATACCTG TTTTTGGTTG TTTTATTTTA TTTTTTTTTT CTATTAAACT GTCAGTGTTG    6300

TGATTGTTGT AATGAACAGT GAGAATATCC CACTCTAAAC TGTGCCCTGG AAAGCTTTTC    6360

AGGTGCATTG GTTTAAAAGA AGGAAGTGTT CTATAGGTGA ACACTTCAAA ACCCAGATCA    6420

GCCAAGATTC ATTGTAAATC CATTTGTTTT CCCTCTTTAA CATGGGCAAT AATGTCAAAT    6480

GTGCTATGCA GCAGTTAATA TTTTAGAAGA TTTGAATGAC TTTATTAACA GAATTGTTAC    6540

AATGCACACT GATTGTACAT AGATAACTTC TATCTGACAA ATTAAATTAA CTAAAACCAA    6600

AAAAAACC                                                           6608
```

(2) INFORMATION FOR SEQ ID NO: 11:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 88 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Asp Glu Ile Val Ser Val Lys His Leu His Lys Lys Ile Lys Thr Glu
1   5   10   15

Lys Glu Asn Glu Glu Lys Pro Glu Pro Asp Ile Gly Ile Lys Lys Glu
                20   25   30

Ala Glu Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys Arg Glu Leu
                35   40   45

Lys Arg Glu Lys Lys Glu Lys Glu Asp Lys Lys Glu Leu Lys Glu Lys
                50   55   60

Asp Asn Lys Glu Lys Arg Glu Asn Lys Val Lys Glu Ser Thr Gln Lys
65   70   75   80

Glu Lys Glu Val Lys Glu Glu Lys
                85

(2) INFORMATION FOR SEQ ID NO: 12:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 265 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GATGAGATTG TTTCAGTGAA ACATCTACAT AAAAAAATAA AAACAGAAAA AAGAAAATGA   60

AGAAAAGCCT GAGCCAGATA TTGGTATAAA GAAGGAAGCT GAAGAAAAAA GAGAGACAAA   120

AGAGAAGGAA AATAAAAGGG AATTGAAAAG GGAGAAAAAA GAAAAGAGG ATAAGAAAGA   180

ATTAAAAGAA AAAGATAATA AAGAAAGAG AGAAAACAAA GTAAAAGAAT CCACACAGAA   240

AGAAAAAGAA GTGAAGGAAG AGAAG   265

(2) INFORMATION FOR SEQ ID NO: 13:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 137 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GATGGGATTG TTTCAGTGAA ACATCCACAT AAAAAAATAA AAGCAGAAAA AAGAAAATGA   60

AGAAAAAGAT GAGCCAGAGA TTGGTATAAA GAAGGAAGCT GGAGAAAAAA GAGAGACAAA   120

AGAAAAGGAA AATAAGA   137

(2) INFORMATION FOR SEQ ID NO: 14:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 45 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
Asp Gly Ile Val Ser Val Lys His Pro His Lys Lys Ile Lys Ala Glu
1               5                   10                  15
Lys Glu Asn Glu Glu Lys Asp Glu Pro Glu Ile Gly Ile Lys Lys Glu
            20                  25                  30
Ala Gly Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO: 15:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1316 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```
ATTTATCGGC TAGTCACAAA AGGATCAGTA GAAGAAGATA TTCTTGAAAG AGCCAAGAAA    60
AAGATGGTGT TAGATCATTT AGTGATTCAG AGAATGGACA CCACAGGGAA AACTGTACTA   120
CATACAGGCT CTACTCCTTC AAGCTCAACA CCTTTTAATA AGGAAGAGTT ATCAGCAATT   180
TTGAAGTTTG GTGCTGAGGA ACTTTTTAAA GAACCTGAAN NNGAAGAAGA GGAGCCTCAG   240
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAAACTC GAGAAAATGA GTCAGGCCCA   300
TTAACTGTAG GAGATGAGTT ACTTTCACAG TTCAAGGTAG CTAACTTTTC CAATATGGAT   360
GAAGATGACA TTGAATTGGA ACCAGAACAA AATCTAAGAA ACTGGGAAGA AATCATTCCA   420
GAAGTTCAGT GGCGACGAAT AGAGGGGNNG GAAAGACAAA AGAACTTGA AGAAATATAT   480
ATGCTTCCAA GAATGAGAAA CTGTGCAAAA CAGATCAGCT TTAATGGAAA TGAAGGGAGA   540
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TGCAGTAGGA GCAGAAGATA TTCTGGATCT GATAGTGATT CCATCTCAGA AAGAAAACGA 600

CCAAAAAAAC GTGGACGACC ACGAACTATT CCCCGTGAAA ACATTAAAGG ATTTAGTGAT 660

GCAGAGATTA GACGATTTAT CAAGAGTTAC AAGAAATTTG GTGGCCCAGT TGAAAGGTTA 720

GATGCTATAG CTAGAGATGC TGAGCTAGTT GATAAATCTG AAACAGACCT TAGACGTCTG 780

GGAGAACTTG TACATAATGG ATGCATTAAG GCTTTAAATG ATAATGACTT TGGTCAAGGA 840

AGAACAGGTG GTAGATTTGG GAAAGTTAAA GGCCCAACAT TCCGAATAGC AGGAGTGCAG 900

GTGAATGCAA AGCTAGTCAT TTCTCACGAA GAAGAGTTGG CACCATTGCA TAAATCGATT 960

CCTTCAGATC CAGAAGAAAG GAAAGATATT GTCATCCCAT ACCACACCAA AGCAGCTCAT 1020

TTTGATATAG ATTGGGGTAA AGAAGATGAT TCCAATCTGT TAATAGGCAT CTATGAATAT 1080

GGTTATGGCA GTTGGGAAAT GATAAAAATG GATCCTGATC TCAGTTTGAC ACAGAAGATT 1140

TTACCTGATG ATCCAGATAA GAAACCCCAG GCTAAGCAGT TACAGACTCG TGCAGATTAC 1200

CTCATTAAAT TACTGAATAA AGACCTTGCA AGAAAGGAAG CACAGAGACT TGCTGGTGCA 1260

GGCAATTCAA AGAGGAGAAA AACAAGAAGT AAGAAGAATA AAGCAACAAA GGCTGC 1316

(2) INFORMATION FOR SEQ ID NO: 16:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 2108 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Asp Ala Arg Arg Tyr Leu Gly Lys Asn Leu Gly His Leu Arg Ile Ala

1   5   10   15

Ser Gln Thr His Tyr Phe Glu Asn Ile Arg Ser Thr Arg Lys Gly Ile

```
                    20                      25                      30
      Leu Asp Leu His Leu Val Thr Val Asp Phe Leu Phe Asn Phe Leu Ile
              35                      40                      45
      Leu Thr Met Asn Gly His Ser Asp Glu Glu Ser Val Arg Asn Ser Ser
          50                      55                      60
      Gly Glu Ser Ser Arg Ser Asp Asp Asp Ser Ala Gly Ser Ala Ser Gly
      65                      70                      75                      80
      Ser Gly Ser Gly Ser Ser Ser Gly Ser Ser Ser Asp Gly Ser Ser Ser
                      85                      90                      95
      Gln Ser Gly Ser Ser Asp Ser Glu Ser Gly Ser Glu Ser Gly Ser Gln
                  100                     105                     110
      Ser Glu Ser Glu Ser Asp Thr Ser Arg Glu Lys Lys Gln Val Gln Ala
                  115                     120                     125
      Lys Pro Pro Lys Ala Asp Gly Ser Glu Phe Trp Lys Ser Ser Pro Ser
              130                     135                     140
      Ile Leu Ala Val Gln Arg Ser Ala Val Leu Lys Lys Gln Gln Gln Gln
      145                     150                     155                     160
      Gln Lys Ala Ala Ser Ser Asp Ser Gly Ser Glu Glu Asp Ser Ser Ser
                      165                     170                     175
      Ser Glu Asp Ser Ala Asp Asp Ser Ser Ser Glu Thr Lys Lys Lys Lys
                  180                     185                     190
      His Lys Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Val Ser Gly
              195                     200                     205
      Thr Gly Ser Asp Ser Glu Ser Ala Glu Asp Gly Asp Lys Ser Ser Cys
              210                     215                     220
```

Glu Glu Ser Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg
225   230   235   240

Lys Pro Pro Ser Arg Ile Lys Pro Lys Ser Gly Lys Lys Ser Thr Gly
                245   250   255

Gln Lys Lys Arg Gln Leu Asp Ser Ser Glu Glu Glu Glu Asp Asp Asp
                260   265   270

Glu Asp Tyr Asp Lys Arg Gly Ser Arg Arg Gln Ala Thr Val Asn Val
                275   280   285

Ser Tyr Lys Glu Ala Glu Glu Thr Lys Thr Asp Ser Asp Asp Leu Leu
290   295   300

Glu Val Cys Gly Glu Asp Val Pro Gln Thr Glu Glu Asp Glu Phe Glu
305   310   315   320

Thr Ile Glu Lys Phe Met Asp Ser Arg Ile Gly Arg Lys Gly Ala Thr
                325   330   335

Gly Ala Ser Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn
                340   345   350

Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile
                355   360   365

Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu
370   375   380

Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr
385   390   395   400

Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro
                405   410   415

Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu

```
                420                    425                     430
His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln
          435                    440                     445
Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu
        450                    455                     460
Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys
465                    470                    475                    480
Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr
                485                    490                     495
Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val
          500                    505                     510
Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu
          515                    520                     525
Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp
        530                    535                     540
Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys
545                    550                    555                    560
Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln
                565                    570                     575
Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser
                580                    585                     590
Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val
          595                    600                     605
Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp
        610                    615                     620
```

Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr
625   630   635   640

Tyr Glu Ile Leu Leu Lys Asp Lys Ser Phe Leu Gly Gly Leu Asn Trp
            645   650   655

Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser
            660   665   670

Leu Leu Tyr Arg Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu
         675   680   685

Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu
     690   695   700

Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu
705   710   715   720

Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys
            725   730   735

Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys
            740   745   750

Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala
         755   760   765

Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala
         770   775   780

Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met
785   790   795   800

Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro
            805   810   815

Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile

```
                 820                      825                      830
Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu
             835                      840                      845
Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met
         850                      855                      860
Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln
865                      870                      875                      880
Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp
                     885                      890                      895
His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr
                 900                      905                      910
Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val
             915                      920                      925
Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala
         930                      935                      940
Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu
945                      950                      955                      960
Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys
                     965                      970                      975
Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly
                 980                      985                      990
Lys Thr Val Leu His Thr Gly Ser Ala Pro Ser Ser Ser Thr Pro Phe
             995                     1000                     1005
Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu
         1010                     1015                     1020
```

Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile
1025   1030   1035   1040

Asp Glu Ile Leu Lys Arg Ala Glu Thr His Glu Asn Glu Pro Gly Pro
              1045   1050   1055

Leu Ser Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe
              1060   1065   1070

Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser
              1075   1080   1085

Lys Asn Trp Glu Glu Ile Ile Pro Glu Glu Gln Arg Arg Arg Leu Glu
              1090   1095   1100

Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg
1105   1110   1115   1120

Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg
              1125   1130   1135

Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Ser
              1140   1145   1150

Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg
              1155   1160   1165

Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys
              1170   1175   1180

Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Ile Ala
1185   1190   1195   1200

Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu
              1205   1210   1215

Gly Glu Leu Val His Asn Gly Cys Val Lys Ala Leu Lys Asp Ser Ser

<pre>
              1220   1225   1230
Ser Gly Thr Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro
         1235   1240   1245
Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ala
      1250   1255   1260
His Glu Asp Glu Leu Ile Pro Leu His Lys Ser Ile Pro Ser Asp Pro
1265   1270   1275   1280
Glu Glu Arg Lys Gln Tyr Thr Ile Pro Cys His Thr Lys Ala Ala His
                   1285   1290   1295
Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Ile Gly
              1300   1305   1310
Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro
         1315   1320   1325
Asp Leu Ser Leu Thr His Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys
      1330   1335   1340
Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu
1345   1350   1355   1360
Leu Ser Arg Asp Leu Ala Lys Arg Glu Ala Gln Arg Leu Cys Gly Ala
                   1365   1370   1375
Gly Gly Ser Lys Arg Arg Lys Thr Arg Ala Lys Lys Ser Lys Ala Met
              1380   1385   1390
Lys Ser Ile Lys Val Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Leu
         1395   1400   1405
Pro Ser Glu Lys Ser Asp Glu Asp Asp Asp Lys Leu Asn Asp Ser Lys
      1410   1415   1420
</pre>

Pro Glu Ser Lys Asp Arg Ser Lys Lys Ser Val Val Ser Asp Ala Pro
1425   1430   1435   1440

Val His Ile Thr Ala Ser Gly Glu Pro Val Pro Ile Ala Glu Glu Ser
                1445   1450   1455

Glu Glu Leu Asp Gln Lys Thr Phe Ser Ile Cys Lys Glu Arg Met Arg
                1460   1465   1470

Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu Lys Gly Leu
                1475   1480   1485

Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu Ile Lys Ile
                1490   1495   1500

Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Ser Asn Pro Glu Gln
1505   1510   1515   1520

Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser Lys Phe Thr
                1525   1530   1535

Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His Ala Ile Lys
                1540   1545   1550

Lys Arg Gln Glu Ser Gln Gln Asn Ser Asp Gln Asn Ser Asn Val Ala
                1555   1560   1565

Thr Thr His Val Ile Arg Asn Pro Asp Met Glu Arg Leu Lys Glu Asn
                1570   1575   1580

Thr Asn His Asp Asp Ser Ser Arg Asp Ser Tyr Ser Ser Asp Arg His
1585   1590   1595   1600

Leu Ser Gln Tyr His Asp His His Lys Asp Arg His Gln Gly Asp Ser
                1605   1610   1615

Tyr Lys Lys Ser Asp Ser Arg Lys Arg Pro Tyr Ser Ser Phe Ser Asn

1620   1625   1630

Gly Lys Asp His Arg Glu Trp Asp His Tyr Arg Gln Asp Ser Arg Tyr

        1635   1640   1645

Tyr Ser Asp Arg Glu Lys His Arg Lys Leu Asp Asp His Arg Ser Arg

        1650   1655   1660

Glu His Arg Pro Ser Leu Glu Gly Gly Leu Lys Asp Leu Asp Gln Arg

1665   1670   1675   1680

Ser Pro Tyr Gly Ser Arg Ser Pro Phe Glu His Ser Ala Glu His Arg

                1685   1690   1695

Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Lys Leu

            1700   1705   1710

Met Ser Leu Ser Ser Gly Thr Leu Phe Xaa Pro Leu Thr Xaa Leu Glu

                1715   1720   1725

Arg Tyr Gly Leu Asp Ile Leu Ser Val Ala Val Leu Leu Leu Leu Ser

        1730   1735   1740

Arg Met Gln Gly Leu Leu Ser Gln Gln Lys Lys Asn Ile Phe Val Phe

1745   1750   1755   1760

Lys Val Tyr Ala Ala Leu Cys Cys Lys Cys Cys Gly Thr Phe Phe Leu

                1765   1770   1775

Arg Asn Gly Arg Cys Leu Leu Leu Gln Gly Pro Gln His Cys Pro Phe

                1780   1785   1790

Gln Thr Gly Ser Tyr Tyr Lys Thr Leu His Val Lys Val Val Leu Gly

            1795   1800   1805

Xaa Thr Gln Ile Lys Leu Cys Leu Xaa Met Asn Thr Xaa Thr Leu Thr

        1810   1815   1820

Cys Ala Tyr Val Ser Gly Lys Asn Gly Gly Phe Ile Leu Phe Tyr Phe
1825   1830   1835   1840

Leu Val Glu Asn Ser Gln Gly Leu Cys Ser Leu Ser Lys Ala Thr Cys
                 1845   1850   1855

Leu His Cys Thr Leu Arg Pro Pro Cys Arg Phe Ser Ser Gln Ala Xaa
                 1860   1865   1870

Ile Phe Lys Phe Cys Thr Tyr Ser Cys Lys Ile Ala Arg Ile Ser Pro
                 1875   1880   1885

Val Cys Asp Gln Leu Xaa Cys Leu Phe Met Lys Gln Thr Asn Lys Gln
        1890   1895   1900

Lys Thr Ile Lys Lys Lys Asn Thr Thr Lys Pro Thr Asn Gly Cys Lys
1905   1910   1915   1920

Leu Leu Xaa Ile Asn Xaa Met Ser Phe Phe Pro Ser Gly Phe Phe Trp
                 1925   1930   1935

Leu Phe Leu Ser Pro Thr Thr Gln Ala Phe Phe Ser Gln Ser Gln Tyr
                 1940   1945   1950

Thr Tyr Met Phe Xaa Xaa Asn Ile Ser Met Glu Ser Glu Cys Lys Asn
        1955   1960   1965

Gly Glu Gly Asn Ile Leu Phe His Leu Val Leu Leu Phe Tyr Trp Ile
        1970   1975   1980

Leu Leu His Thr Cys Phe Trp Leu Phe Tyr Phe Ile Phe Phe Phe Tyr
1985   1990   1995   2000

Xaa Thr Val Ser Val Val Ile Val Val Met Asn Ser Glu Asn Ile Pro
                 2005   2010   2015

Leu Xaa Thr Val Pro Trp Lys Ala Phe Gln Val His Trp Phe Lys Arg

```
              2020                  2025                  2030

Arg Lys Cys Ser Ile Gly Glu His Phe Lys Thr Gln Ile Ser Gln Asp

         2035                  2040                  2045

Ser Leu Xaa Ile His Leu Phe Ser Leu Phe Asn Met Gly Asn Asn Val

      2050                  2055                  2060

Lys Cys Ala Met Gln Gln Leu Ile Phe Xaa Lys Ile Xaa Met Thr Leu

2065                  2070                  2075                  2080

Leu Thr Glu Leu Leu Gln Cys Thr Leu Ile Val His Arg Xaa Leu Leu

              2085                  2090                  2095

Ser Asp Lys Leu Asn Xaa Leu Lys Pro Lys Lys Thr

         2100                  2105
```

(2) INFORMATION FOR SEQ ID NO: 17:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 1795 amino acids

      (B) TYPE: amino acid

      (C) STRANDEDNESS:

      (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```
Phe Ala Leu Cys Pro Pro Val Thr Gln Arg Glu Pro Gln Glu Thr Arg
1               5                   10                  15

Glu Cys Arg Lys Phe Ile Phe Glu Ile Leu Ile Phe Glu Glu Ile Cys
              20                  25                  30

Ile His Thr His Leu Leu Leu Ile Gly Asp Phe Cys Phe Ile Asn Phe
```

```
                  35                        40                        45
Leu Ile Phe Thr Met Asn Gly His Ser Asp Glu Glu Ser Val Arg Asn
          50                        55                        60
Gly Ser Gly Glu Ser Ser Gln Ser Gly Asp Asp Cys Gly Ser Ala Ser
      65                        70                        75              80
Gly Ser Gly Ser Gly Ser Ser Ser Gly Ser Ser Ser Asp Gly Ser Ser
                      85                        90                  95
Ser Gln Ser Gly Ser Ser Asp Ser Asp Ser Gly Ser Asp Ser Gly Ser
                  100                       105                   110
Gln Ser Glu Ser Glu Ser Asp Thr Ser Arg Glu Asn Lys Val Gln Ala
              115                       120                   125
Lys Pro Pro Lys Val Asp Gly Ala Glu Phe Trp Lys Ser Ser Pro Ser
          130                       135                   140
Ile Leu Ala Val Gln Arg Ser Ala Met Leu Arg Lys Gln Pro Gln Gln
145                       150                       155                   160
Ala Gln Gln Gln Arg Pro Ala Ser Ser Asn Ser Gly Ser Glu Glu Asp
                      165                       170                   175
Ser Ser Ser Ser Glu Asp Ser Asp Asp Ser Ser Ser Gly Ala Lys Arg
                  180                       185                   190
Lys Lys His Asn Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Pro
              195                       200                   205
Ser Gln Leu Gly Ser Asp Ser Glu Ser Glu Glu Glu Arg Asp Lys Ser
          210                       215                   220
Ser Cys Asp Gly Thr Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Arg
225                       230                       235                   240
```

Ser Arg Lys Pro Gln Asn Arg Ser Lys Ser Lys Asn Gly Lys Lys Ile
                245   250   255

Leu Gly Gln Lys Lys Arg Gln Ile Asp Ser Ser Glu Asp Glu Asp Asp
                260   265   270

Glu Asp Tyr Asp Asn Asp Lys Arg Ser Ser Arg Arg Gln Ala Thr Val
                275   280   285

Asn Val Ser Tyr Lys Glu Asp Glu Glu Met Lys Thr Asp Ser Asp Asp
        290   295   300

Leu Leu Glu Val Cys Gly Glu Asp Val Pro Gln Pro Glu Asp Glu Glu
305   310   315   320

Phe Glu Thr Ile Glu Arg Val Met Asp Cys Arg Val Gly Arg Lys Gly
                325   330   335

Ala Thr Gly Ala Thr Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp
                340   345   350

Pro Asn Ala Gly Phe Glu Arg Asn Lys Glu Pro Gly Asp Ile Gln Tyr
                355   360   365

Leu Ile Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr
        370   375   380

Glu Glu Thr Leu Lys Gln Gln Asn Val Arg Gly Met Lys Lys Leu Asp
385   390   395   400

Asn Tyr Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala
                405   410   415

Ser Pro Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp
                420   425   430

Asp Leu His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser

                435   440   445

Asn Gln Lys Ser Ala Ala Gly Leu Pro Asp Tyr Tyr Cys Lys Trp Gln
    450   455   460

Gly Leu Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ser
465   470   475   480

Lys Lys Phe Gln Thr Cys Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser
                485   490   495

Lys Thr Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg
            500   505   510

Phe Val Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Gly
        515   520   525

Leu Glu Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His
    530   535   540

Ser Trp Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu
545   550   555   560

Gly Lys Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu
                565   570   575

His Gln Leu Tyr Gly Pro Phe Leu Leu Val Val Pro Leu Ser Thr Leu
            580   585   590

Thr Ser Trp Gln Arg Glu Ile Gln Thr Trp Ala Ser Gln Met Asn Ala
        595   600   605

Val Val Tyr Leu Gly Asp Ile Asn Ser Arg Asn Met Ile Arg Thr His
    610   615   620

Glu Trp Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu
625   630   635   640

Thr Thr Tyr Glu Ile Leu Leu Lys Asp Lys Ala Phe Leu Gly Gly Leu
                    645   650   655

Asn Trp Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp
                    660   665   670

Asp Ser Leu Leu Tyr Lys Thr Leu Ile Asp Phe Lys Ser Asn His Arg
                675   680   685

Leu Leu Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp
            690   695   700

Ser Leu Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp
705   710   715   720

Phe Glu Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu
                    725   730   735

His Lys Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val
                740   745   750

Glu Lys Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met
                755   760   765

Ser Ala Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr
        770   775   780

Lys Ala Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn
785   790   795   800

Ile Met Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys
                    805   810   815

Pro Pro Asp Asn Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His
                820   825   830

Leu Ile Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile

```
              835                    840                    845
Arg Leu Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val
         850                    855                    860
Arg Met Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro
865                    870                    875                    880
Phe Gln Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala
                   885                    890                    895
Leu Asp His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu
                   900                    905                    910
Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr
         915                    920                    925
Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala
         930                    935                    940
Gln Ala Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr
945                    950                    955                    960
Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala
                   965                    970                    975
Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr
                   980                    985                    990
Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr
              995                    1000                   1005
Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu
         1010                   1015                   1020
Glu Leu Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met
1025                   1030                   1035                   1040
```

Asp Ile Asp Glu Ile Leu Lys Arg Ala Glu Thr Arg Glu Asn Glu Pro
                1045   1050   1055

Gly Pro Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala
                1060   1065   1070

Asn Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg
              1075   1080   1085

Asn Ser Arg Asn Trp Glu Glu Ile Ile Pro Glu Ser Gln Arg Arg Arg
            1090   1095   1100

Ile Glu Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu
1105   1110   1115   1120

Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu
                1125   1130   1135

Gly Arg Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser
              1140   1145   1150

Ile Thr Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile
            1155   1160   1165

Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe
    1170   1175   1180

Ile Lys Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala
1185   1190   1195   1200

Val Ala Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg
                1205   1210   1215

Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp
              1220   1225   1230

Asn Ser Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys

```
           1235                    1240                    1245
Gly Pro Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val
          1250                    1255                    1260
Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser
    1265                    1270                    1275                    1280
Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala
                    1285                    1290                    1295
Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu
                    1300                    1305                    1310
Val Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met
          1315                    1320                    1325
Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp
          1330                    1335                    1340
Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile
    1345                    1350                    1355                    1360
Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala
                    1365                    1370                    1375
Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys
                    1380                    1385                    1390
Met Lys Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro
          1395                    1400                    1405
Gln Pro Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Glu Asp Asn Lys
          1410                    1415                    1420
Val Asn Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro
    1425                    1430                    1435                    1440
```

Leu Leu Asp Thr Pro Val His Ile Thr Ala Thr Ser Glu Pro Val Pro
            1445   1450   1455

Ile Ser Glu Glu Ser Glu Glu Leu His Gln Lys Thr Phe Ser Val Cys
            1460   1465   1470

Lys Glu Arg Met Arg Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg
            1475   1480   1485

Pro Glu Lys Gly Leu Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln
            1490   1495   1500

Cys Leu Ile Lys Ile Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr
1505   1510   1515   1520

Thr Asn Pro Glu Gln Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe
            1525   1530   1535

Val Ser Lys Phe Thr Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr
            1540   1545   1550

Lys His Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln His Asn Asp Gln
            1555   1560   1565

Asn Ile Ser Ser Asn Val Asn Thr His Val Ile Arg Asn Pro Asp Val
            1570   1575   1580

Glu Arg Leu Lys Glu Thr Thr Asn His Asp Asp Ser Ser Arg Asp Ser
1585   1590   1595   1600

Tyr Ser Ser Asp Arg His Leu Ser Gln Tyr His Asp His His Lys Asp
            1605   1610   1615

Arg His Gln Gly Asp Ala Tyr Lys Lys Ser Asp Ser Arg Lys Arg Pro
            1620   1625   1630

Tyr Ser Ala Phe Ser Asn Gly Lys Asp His Arg Asp Trp Asp His Tyr

```
              1635                    1640                      1645

Lys Gln Asp Ser Arg Tyr Tyr Ser Asp Ser Lys His Arg Lys Leu Asp

        1650                  1655                      1660

Asp His Arg Ser Arg Asp His Arg Ser Asn Leu Glu Gly Asn Leu Lys

  1665                 1670                  1675                    1680

Asp Ser Arg Gly His Ser Asp His Arg Ser His Ser Asp His Arg Ile

                1685                  1690                      1695

His Ser Asp His Arg Ser Thr Ser Glu Tyr Ser His His Lys Ser Ser

              1700                  1705                      1710

Arg Asp Tyr Arg Tyr His Ser Asp Trp Gln Met Asp His Arg Ala Ser

        1715                  1720                      1725

Gly Ser Gly Pro Arg Ser Pro Leu Asp Gln Arg Ser Pro Tyr Gly Ser

        1730                  1735                      1740

Arg Ser Pro Leu Gly His Arg Ser Pro Phe Glu His Ser Ser Asp His

  1745                 1750                  1755                    1760

Lys Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Arg

                1765                  1770                      1775

Leu Thr Phe Ser Gly Pro Ser Phe Xaa Pro Tyr Thr Val Asn Xaa His

              1780                  1785                      1790

Ser Asn Cys

        1795
```

(2) INFORMATION FOR SEQ ID NO: 18:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 99 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```
Lys Thr Xaa Glu Pro Gly Glu Ile Gln Tyr Leu Ile Lys Trp Lys Gly
1               5                   10                  15

Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln
                20                  25                  30

Gln Asn Val Arg Gly Met Lys Lys Leu Asp Asn Tyr Lys Lys Lys Asp
                35                  40                  45

Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro Glu Asp Val Glu
        50                  55                  60

Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu His Lys Gln Tyr
65                  70                  75                  80

Gln Ile Val Glu Arg Thr Asn Xaa Ser Phe Gln Ser Lys Ser Ala Ala
                85                  90                  95

Gly Tyr Pro
```

(2) INFORMATION FOR SEQ ID NO: 19:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 439 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Ile Tyr Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu
1   5   10   15

Arg Ala Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met
            20   25   30

Asp Thr Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser
            35   40   45

Ser Thr Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly
        50   55   60

Ala Glu Glu Leu Phe Lys Glu Pro Glu Xaa Glu Glu Glu Glu Pro Gln
65   70   75   80

Glu Met Asp Ile Asp Glu Ile Leu Lys Arg Xaa Glu Thr Arg Glu Asn
                85   90   95

Glu Ser Gly Pro Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys
            100   105   110

Val Ala Asn Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro
            115   120   125

Glu Gln Asn Leu Arg Asn Trp Glu Glu Ile Ile Pro Glu Val Gln Trp
        130   135   140

Arg Arg Ile Glu Gly Xaa Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr
145   150   155   160

Met Leu Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly
            165   170   175

Asn Glu Gly Arg Cys Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser

```
                  180                      185                      190
Asp Ser Ile Ser Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg
                  195                      200                      205
Thr Ile Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg
                  210                      215                      220
Arg Phe Ile Lys Ser Tyr Lys Lys Phe Gly Gly Pro Val Glu Arg Leu
225                      230                      235                      240
Asp Ala Ile Ala Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp
                  245                      250                      255
Leu Arg Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu
                  260                      265                      270
Asn Asp Asn Asp Phe Gly Gln Gly Arg Thr Gly Gly Arg Phe Gly Lys
                  275                      280                      285
Val Lys Gly Pro Thr Phe Arg Ile Ala Gly Val Gln Val Asn Ala Lys
                  290                      295                      300
Leu Val Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile
305                      310                      315                      320
Pro Ser Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Tyr His Thr
                  325                      330                      335
Lys Ala Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn
                  340                      345                      350
Leu Leu Ile Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile
                  355                      360                      365
Lys Met Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp
                  370                      375                      380
```

```
Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr
385                 390                 395                 400

Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg
                405                 410                 415

Leu Ala Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Ser Lys Lys
                420                 425                 430

Asn Lys Ala Thr Lys Ala Ala
        435
```

(2) INFORMATION FOR SEQ ID NO: 20:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1434 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:

        (A) NAME/KEY: Peptide

        (B) LOCATION:1..1434

        (D) OTHER INFORMATION:/note= "The sequence beginning at 1
           corresponds to 55 and that ending at 1434 corresponds to
1488"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```
Lys Pro Pro Lys Ala Asp Gly Ser Glu Phe Trp Lys Ser Ser Pro Ser
1               5               10                  15
```

Ile Leu Ala Val Gln Arg Ser Ala Val Leu Lys Lys Gln Gln Gln Gln
          20   25   30

Gln Lys Ala Ala Ser Ser Asp Ser Gly Ser Glu Glu Asp Ser Ser Ser
          35   40   45

Ser Glu Asp Ser Ala Asp Asp Ser Ser Ser Glu Thr Lys Lys Lys Lys
        50   55   60

His Lys Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Val Ser Gly
65   70   75   80

Thr Gly Ser Asp Ser Glu Ser Ala Glu Asp Gly Asp Lys Ser Ser Cys
              85   90   95

Glu Glu Ser Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg
          100   105   110

Lys Pro Pro Ser Arg Ile Lys Pro Lys Ser Gly Lys Lys Ser Thr Gly
          115   120   125

Gln Lys Lys Arg Gln Leu Asp Ser Ser Glu Glu Glu Asp Asp Asp
    130   135   140

Glu Asp Tyr Asp Lys Arg Gly Ser Arg Arg Gln Ala Thr Val Asn Val
145   150   155   160

Ser Tyr Lys Glu Ala Glu Glu Thr Lys Thr Asp Ser Asp Asp Leu Leu
              165   170   175

Glu Val Cys Gly Glu Asp Val Pro Gln Thr Glu Glu Asp Glu Phe Glu
          180   185   190

Thr Ile Glu Lys Phe Met Asp Ser Arg Ile Gly Arg Lys Gly Ala Thr
          195   200   205

Gly Ala Ser Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn

                210   215   220
Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile
225   230   235   240
Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu
                        245   250   255
Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr
                        260   265   270
Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro
                275   280   285
Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu
                290   295   300
His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln
305   310   315   320
Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu
                        325   330   335
Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys
                        340   345   350
Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr
                355   360   365
Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val
                370   375   380
Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu
385   390   395   400
Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp
                        405   410   415

Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys
          420   425   430

Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln
              435   440   445

Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser
      450   455   460

Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val
465   470   475   480

Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp
                  485   490   495

Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr
              500   505   510

Tyr Glu Ile Leu Leu Lys Asp Lys Ser Phe Leu Gly Gly Leu Asn Trp
          515   520   525

Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser
      530   535   540

Leu Leu Tyr Arg Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu
545   550   555   560

Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu
                  565   570   575

Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu
              580   585   590

Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys
          595   600   605

Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys

610   615   620

Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala

625   630   635   640

Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala

645   650   655

Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met

660   665   670

Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro

675   680   685

Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile

690   695   700

Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu

705   710   715   720

Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met

725   730   735

Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln

740   745   750

Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp

755   760   765

His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr

770   775   780

Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val

785   790   795   800

Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala

805   810   815

Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu
      820   825   830

Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys
      835   840   845

Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly
      850   855   860

Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr Pro Phe
865   870   875   880

Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu
          885   890   895

Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile
          900   905   910

Asp Glu Ile Leu Lys Arg Ala Glu Thr Arg Glu Asn Glu Pro Gly Pro
          915   920   925

Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe
          930   935   940

Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser
945   950   955   960

Arg Asn Trp Glu Glu Ile Ile Pro Glu Ser Gln Arg Arg Arg Ile Glu
          965   970   975

Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg
          980   985   990

Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg
      995   1000   1005

Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Thr

                1010   1015   1020

Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg

1025   1030   1035   1040

Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys

                        1045   1050   1055

Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Val Ala

                1060   1065   1070

Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu

                    1075   1080   1085

Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp Asn Ser

            1090   1095   1100

Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro

1105   1110   1115   1120

Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ser

                    1125   1130   1135

His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser Asp Pro

                1140   1145   1150

Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala Ala His

            1155   1160   1165

Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Val Gly

        1170   1175   1180

Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro

1185   1190   1195   1200

Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys

                    1205   1210   1215

Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu
        1220   1225   1230

Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala Gly Ala
        1235   1240   1245

Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys Met Lys
        1250   1255   1260

Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Gln Pro
1265   1270   1275   1280

Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Glu Asp Asn Lys Val Asn
                1285   1290   1295

Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro Leu Leu
                1300   1305   1310

Asp Thr Pro Val His Ile Thr Ala Thr Ser Glu Pro Val Pro Ile Ser
        1315   1320   1325

Glu Glu Ser Glu Glu Leu His Gln Lys Thr Phe Ser Val Cys Lys Glu
        1330   1335   1340

Arg Met Arg Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu
1345   1350   1355   1360

Lys Gly Leu Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu
                1365   1370   1375

Ile Lys Ile Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Thr Asn
                1380   1385   1390

Pro Glu Gln Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser
                1395   1400   1405

Lys Phe Thr Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His

          1410   1415   1420

     Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln

     1425   1430

(2) INFORMATION FOR SEQ ID NO: 21:

    (i) SEQUENCE CHARACTERISTICS:

         (A) LENGTH: 1467 amino acids

         (B) TYPE: amino acid

         (C) STRANDEDNESS:

         (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:

         (A) NAME/KEY: Peptide

         (B) LOCATION:1..1467

         (D) OTHER INFORMATION:/note= "The sequence beginning at 1

              corresponds to 2654 and that ending at 1467 corresponds tc

4120"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

    Met Ala Ala Lys Asp Ile Ser Thr Glu Val Leu Gln Asn Pro Glu Leu

    1   5   10   15

    Tyr Gly Leu Arg Arg Ser His Arg Ala Ala Ala His Gln Gln Asn Tyr

                    20   25   30

    Phe Asn Asp Ser Asp Asp Glu Asp Asp Glu Asp Asn Ile Lys Gln Ser

               35   40   45

    Arg Arg Lys Arg Met Thr Thr Ile Glu Asp Asp Glu Asp Glu Phe Glu

```
              50                        55                        60
Asp Glu Glu Gly Glu Glu Asp Ser Gly Glu Asp Glu Asp Glu Glu Asp
65                        70                        75                        80
Phe Glu Glu Asp Asp Asp Tyr Tyr Gly Ser Pro Ile Lys Gln Asn Arg
                      85                        90                        95
Ser Lys Pro Lys Ser Arg Thr Lys Ser Lys Ser Lys Ser Lys Pro Lys
                  100                       105                       110
Ser Gln Ser Glu Lys Gln Ser Thr Val Lys Ile Pro Thr Arg Phe Ser
              115                       120                       125
Asn Arg Gln Asn Lys Thr Val Asn Tyr Asn Ile Asp Tyr Ser Asp Asp
          130                       135                       140
Asp Leu Leu Glu Ser Glu Asp Asp Tyr Gly Ser Glu Glu Ala Leu Ser
145                       150                       155                       160
Glu Glu Asn Val His Glu Ala Ser Ala Asn Pro Gln Pro Glu Asp Phe
                  165                       170                       175
His Gly Ile Asp Ile Val Ile Asn His Arg Leu Lys Thr Ser Leu Glu
                  180                       185                       190
Glu Gly Lys Val Leu Glu Lys Thr Val Pro Asp Leu Asn Asn Cys Lys
              195                       200                       205
Glu Asn Tyr Glu Phe Leu Ile Lys Trp Thr Asp Glu Ser His Leu His
          210                       215                       220
Asn Thr Trp Glu Thr Tyr Glu Ser Ile Gly Gln Val Arg Gly Leu Lys
225                       230                       235                       240
Arg Leu Asp Asn Tyr Cys Lys Gln Phe Ile Ile Glu Asp Gln Gln Val
                  245                       250                       255
```

Arg Leu Asp Pro Tyr Val Thr Ala Glu Asp Ile Glu Ile Met Asp Met
              260   265   270

Glu Arg Glu Arg Arg Leu Asp Glu Phe Glu Glu Phe His Val Pro Glu
          275   280   285

Arg Ile Ile Asp Ser Gln Arg Ala Ser Leu Glu Asp Gly Thr Ser Gln
      290   295   300

Leu Gln Tyr Leu Val Lys Trp Arg Arg Leu Asn Tyr Asp Glu Ala Thr
305   310   315   320

Trp Glu Asn Ala Thr Asp Ile Val Lys Leu Ala Pro Glu Gln Val Lys
              325   330   335

His Phe Gln Asn Arg Glu Asn Ser Lys Ile Leu Pro Gln Tyr Ser Ser
              340   345   350

Asn Tyr Thr Ser Gln Arg Pro Arg Phe Glu Lys Leu Ser Val Gln Pro
              355   360   365

Pro Phe Ile Lys Gly Gly Glu Leu Arg Asp Phe Gln Leu Thr Gly Ile
      370   375   380

Asn Trp Met Ala Phe Leu Trp Ser Lys Gly Asp Asn Gly Ile Leu Ala
385   390   395   400

Asp Glu Met Gly Leu Gly Lys Thr Val Gln Thr Val Ala Phe Ile Ser
              405   410   415

Trp Leu Ile Phe Ala Arg Arg Gln Asn Gly Pro His Ile Ile Val Val
              420   425   430

Pro Leu Ser Thr Met Pro Ala Trp Leu Asp Thr Phe Glu Lys Trp Ala
          435   440   445

Pro Asp Leu Asn Cys Ile Cys Tyr Met Gly Asn Gln Lys Ser Arg Asp

```
        450                    455                    460
Thr Ile Arg Glu Tyr Glu Phe Tyr Thr Asn Pro Arg Ala Lys Gly Lys
465                    470                    475                    480
Lys Thr Met Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Leu
                485                    490                    495
Lys Asp Arg Ala Glu Leu Gly Ser Ile Lys Trp Gln Phe Met Ala Val
                500                    505                    510
Asp Glu Ala His Arg Leu Lys Asn Ala Glu Ser Ser Leu Tyr Glu Ser
                515                    520                    525
Leu Asn Ser Phe Lys Val Ala Asn Arg Met Leu Ile Thr Gly Thr Pro
        530                    535                    540
Leu Gln Asn Asn Ile Lys Glu Leu Ala Ala Leu Val Asn Phe Leu Met
545                    550                    555                    560
Pro Gly Arg Phe Thr Ile Asp Gln Glu Ile Asp Phe Glu Asn Gln Asp
                565                    570                    575
Glu Glu Gln Glu Glu Tyr Ile His Asp Leu His Arg Arg Ile Gln Pro
                580                    585                    590
Phe Ile Leu Arg Arg Leu Lys Lys Asp Val Glu Lys Ser Leu Pro Ser
        595                    600                    605
Lys Thr Glu Arg Ile Leu Arg Val Glu Leu Ser Asp Val Gln Thr Glu
        610                    615                    620
Tyr Tyr Lys Asn Ile Leu Thr Lys Asn Tyr Ser Ala Leu Thr Ala Gly
625                    630                    635                    640
Ala Lys Gly Gly His Phe Ser Leu Leu Asn Ile Met Asn Glu Leu Lys
                645                    650                    655
```

Lys Ala Ser Asn His Pro Tyr Leu Phe Asp Asn Ala Glu Glu Arg Val
            660   665   670

Leu Gln Lys Phe Gly Asp Gly Lys Met Thr Arg Glu Asn Val Leu Arg
            675   680   685

Gly Leu Ile Met Ser Ser Gly Lys Met Val Leu Leu Asp Gln Leu Leu
        690   695   700

Thr Arg Leu Lys Lys Asp Gly His Arg Val Leu Ile Phe Ser Gln Met
705   710   715   720

Val Arg Met Leu Asp Ile Leu Gly Asp Tyr Leu Ser Ile Lys Gly Ile
                725   730   735

Asn Phe Gln Arg Leu Asp Gly Thr Val Pro Ser Ala Gln Arg Arg Ile
            740   745   750

Ser Ile Asp His Phe Asn Ser Pro Asp Ser Asn Asp Phe Val Phe Leu
            755   760   765

Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Met Thr Ala Asp
        770   775   780

Thr Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Ala Asp Leu Gln
785   790   795   800

Ala Met Ala Arg Ala His Arg Ile Gly Gln Lys Asn His Val Met Val
                805   810   815

Tyr Arg Leu Val Ser Lys Asp Thr Val Glu Glu Glu Val Leu Glu Arg
            820   825   830

Ala Arg Lys Lys Met Ile Leu Glu Tyr Ala Ile Ile Ser Leu Gly Val
            835   840   845

Thr Asp Gly Asn Lys Tyr Thr Lys Lys Asn Glu Pro Asn Ala Gly Glu

```
            850                    855                    860
Leu Ser Ala Ile Leu Lys Phe Gly Ala Gly Asn Met Phe Thr Ala Thr
865                    870                    875                    880
Asp Asn Gln Lys Lys Leu Glu Asp Leu Asn Leu Asp Asp Val Leu Asn
                      885                    890                    895
His Ala Glu Asp His Val Thr Thr Pro Asp Leu Gly Glu Ser His Leu
                 900                    905                    910
Gly Gly Glu Glu Phe Leu Lys Gln Phe Glu Val Thr Asp Tyr Lys Ala
                 915                    920                    925
Asp Ile Asp Trp Asp Asp Ile Ile Pro Glu Glu Glu Leu Lys Lys Leu
                 930                    935                    940
Gln Asp Glu Glu Gln Lys Arg Lys Asp Glu Glu Tyr Val Lys Glu Gln
945                    950                    955                    960
Leu Glu Met Met Asn Arg Arg Asp Asn Ala Leu Lys Lys Ile Lys Asn
                 965                    970                    975
Ser Val Asn Gly Asp Gly Thr Ala Ala Asn Ser Asp Ser Asp Asp Asp
                 980                    985                    990
Ser Thr Ser Arg Ser Ser Arg Arg Arg Ala Arg Ala Asn Asp Met Asp
                 995                    1000                   1005
Ser Ile Gly Glu Ser Glu Val Arg Ala Leu Tyr Lys Ala Ile Leu Lys
                 1010                   1015                   1020
Phe Gly Asn Leu Lys Glu Ile Leu Asp Glu Leu Ile Ala Asp Gly Thr
1025                   1030                   1035                   1040
Leu Pro Val Lys Ser Phe Glu Lys Tyr Gly Glu Thr Tyr Asp Glu Met
                 1045                   1050                   1055
```

Met Glu Ala Ala Lys Asp Cys Val His Glu Glu Glu Lys Asn Arg Lys
            1060   1065   1070

Glu Ile Leu Glu Lys Leu Glu Lys His Ala Thr Ala Tyr Arg Ala Lys
          1075   1080   1085

Leu Lys Ser Gly Glu Ile Lys Ala Glu Asn Gln Pro Lys Asp Asn Pro
        1090   1095   1100

Leu Thr Arg Leu Ser Leu Lys Lys Arg Glu Lys Lys Ala Val Leu Phe
1105   1110   1115   1120

Asn Phe Lys Gly Val Lys Ser Leu Asn Ala Glu Ser Leu Leu Ser Arg
          1125   1130   1135

Val Glu Asp Leu Lys Tyr Leu Lys Asn Leu Ile Asn Ser Asn Tyr Lys
          1140   1145   1150

Asp Asp Pro Leu Lys Phe Ser Leu Gly Asn Asn Thr Pro Lys Pro Val
          1155   1160   1165

Gln Asn Trp Ser Ser Asn Trp Thr Lys Glu Glu Asp Glu Lys Leu Leu
     1170   1175   1180

Ile Gly Val Phe Lys Tyr Gly Tyr Gly Ser Trp Thr Gln Ile Arg Asp
1185   1190   1195   1200

Asp Pro Phe Leu Gly Ile Thr Asp Lys Ile Phe Leu Asn Glu Val His
          1205   1210   1215

Asn Pro Val Ala Lys Lys Ser Ala Ser Ser Ser Asp Thr Thr Pro Thr
          1220   1225   1230

Pro Ser Lys Lys Gly Lys Gly Ile Thr Gly Ser Ser Lys Lys Val Pro
        1235   1240   1245

Gly Ala Ile His Leu Gly Arg Arg Val Asp Tyr Leu Leu Ser Phe Leu

1250   1255   1260

Arg Gly Gly Leu Asn Thr Lys Ser Pro Ser Ala Asp Ile Gly Ser Lys

1265   1270   1275   1280

Lys Leu Pro Thr Gly Pro Ser Lys Lys Arg Gln Arg Lys Pro Ala Asn

                        1285   1290   1295

His Ser Lys Ser Met Thr Pro Glu Ile Thr Ser Ser Glu Pro Ala Asn

                        1300   1305   1310

Gly Pro Pro Ser Lys Arg Met Lys Ala Leu Pro Lys Gly Pro Ala Ala

                        1315   1320   1325

Leu Ile Asn Asn Thr Arg Leu Ser Pro Asn Ser Pro Thr Pro Pro Leu

        1330   1335   1340

Lys Ser Lys Val Ser Arg Asp Asn Gly Thr Arg Gln Ser Ser Asn Pro

1345   1350   1355   1360

Ser Ser Gly Ser Ala His Glu Lys Glu Tyr Asp Ser Met Asp Glu Glu

                        1365   1370   1375

Asp Cys Arg His Thr Met Ser Ala Ile Arg Thr Ser Leu Lys Arg Leu

                        1380   1385   1390

Arg Arg Gly Gly Lys Ser Leu Asp Arg Lys Glu Trp Ala Lys Ile Leu

        1395   1400   1405

Lys Thr Glu Leu Thr Thr Ile Gly Asn His Ile Glu Ser Gln Lys Gly

        1410   1415   1420

Ser Ser Arg Lys Ala Ser Pro Glu Lys Tyr Arg Lys His Leu Trp Ser

1425   1430   1435   1440

Tyr Ser Ala Asn Phe Trp Pro Ala Asp Val Lys Ser Thr Lys Leu Met

                        1445   1450   1455

Ala Met Tyr Asp Lys Ile Thr Glu Ser Gln Lys

1460   1465

(2) INFORMATION FOR SEQ ID NO: 22:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 59 amino acids

      (B) TYPE: amino acid

      (C) STRANDEDNESS:

      (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Val Glu Ala Asp Gly Asp Pro Asn Ala Gly Phe Glu Lys Ser Lys

1   5   10   15

Glu Leu Gly Glu Ile Gln Tyr Leu Ile Lys Trp Lys Gly Trp Ser His

   20   25   30

Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln Gln Asn Val

   35   40   45

Lys Gly Met Asn Lys Leu Asp Asn Tyr Lys Lys

50   55

(2) INFORMATION FOR SEQ ID NO: 23:

   (i) SEQUENCE CHARACTERISTICS:

      (A) LENGTH: 59 amino acids

      (B) TYPE: amino acid

      (C) STRANDEDNESS:

```
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

   Ala Val Glu Ala Asp Gly Asp Pro Asn Ala Gly Phe Glu Arg Asn Lys
   1               5                   10                  15

   Glu Pro Gly Asp Ile Gln Tyr Leu Ile Lys Trp Lys Gly Trp Ser His
                   20                  25                  30

   Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln Gln Asn Val
                   35                  40                  45

   Arg Gly Asn Lys Lys Leu Asp Asn Tyr Lys Lys
       50                  55
```

(2) INFORMATION FOR SEQ ID NO: 24:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 55 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
   Glu Gly Lys Val Leu Glu Lys Thr Val Pro Asp Leu Asn Asn Cys Lys
   1               5                   10                  15

   Glu Asn Tyr Glu Phe Leu Ile Lys Trp Thr Asp Glu Ser His Leu His
                   20                  25                  30

   Asn Thr Trp Glu Thr Tyr Glu Ser Ile Gly Gln Val Arg Gly Leu Lys
```

     35   40   45

Arg Leu Asp Asn Tyr Cys Lys

     50   55

(2) INFORMATION FOR SEQ ID NO: 25:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 52 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Glu Glu Glu Glu Glu Tyr Ala Val Glu Lys Ile Ile Asp Arg Arg Val

1   5   10   15

Arg Lys Gly Lys Val Glu Tyr Tyr Leu Lys Trp Lys Gly Tyr Pro Glu

        20   25   30

Thr Glu Asn Thr Trp Glu Pro Glu Asn Asn Leu Asp Cys Gln Asp Leu

        35   40   45

Ile Gln Gln Tyr

     50

(2) INFORMATION FOR SEQ ID NO: 26:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 53 amino acids

    (B) TYPE: amino acid

    (C) STRANDEDNESS:

    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Asp Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val
1   5   10   15

Val Lys Gly Lys Gln Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser
            20   25   30

Glu Glu His Asn Thr Trp Glu Pro Glu Lys Asn Leu Asp Cys Pro Glu
        35   40   45

Leu Ile Ser Glu Phe
    50

(2) INFORMATION FOR SEQ ID NO: 27:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 52 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Glu Glu Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val
1   5   10   15

Val Lys Gly Lys Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser Asp

       20   25   30

Glu Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Asp Leu

       35   40   45

Ile Ala Glu Phe

       50

(2) INFORMATION FOR SEQ ID NO: 28:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 52 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Ala Glu Pro Glu Glu Phe Val Val Glu Lys Val Leu Asp Arg Arg Val

1   5   10   15

Val Asn Gly Lys Val Glu Tyr Phe Leu Lys Trp Lys Gly Phe Thr Asp

       20   25   30

Ala Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Glu Leu

       35   40   45

Ile Glu Asp Phe

       50

(2) INFORMATION FOR SEQ ID NO: 29:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 52 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Pro Val Asp Leu Val Tyr Ala Ala Glu Lys Ile Ile Gln Lys Arg Val
1   5   10   15

Lys Lys Gly Val Val Glu Tyr Arg Val Lys Trp Lys Gly Trp Asn Gln
          20   25   30

Arg Tyr Asn Thr Trp Glu Pro Glu Asn Asn Ile Leu Asp Arg Arg Leu
          35   40   45

Ile Asp Ile Tyr
   50

(2) INFORMATION FOR SEQ ID NO: 30:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 52 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS:

        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Val Gly Glu Gln Val Phe Ala Ala Glu Cys Ile Leu Ser Lys Arg Leu
1   5   10   15

Arg Lys Gly Lys Leu Glu Tyr Leu Val Lys Trp Arg Gly Trp Ser Ser
                20   25   30

Lys His Asn Ser Trp Glu Pro Glu Glu Asn Ile Leu Asp Pro Arg Leu
            35   40   45

Leu Leu Ala Phe
    50

(2) INFORMATION FOR SEQ ID NO: 31:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 111 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AGATATTCTG GATCTGATAG TGATTCAATC TCGGAAAGGA AACGGCCGAA GAAACGTGGG   60
CGACCCCGCA CTATCCCTCG GGAGAATATT AAAGGATTTA GTGATGCGGA G   111

(2) INFORMATION FOR SEQ ID NO: 32:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 111 base pairs

        (B) TYPE: nucleic acid

            (C) STRANDEDNESS: double

            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AGATATTCTG GATCTGATAG TGACTCCATC ACAGAAAGAA AACGGCCAAA AAAGCGTGGA   60

AGACCTCGAA CCATTCCTCG AGAAAATATT AAAGGATTTA GTGATGCAGA G   111

(2) INFORMATION FOR SEQ ID NO: 33:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 67 base pairs

            (B) TYPE: nucleic acid

            (C) STRANDEDNESS: double

            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTCCATCTCG GAAAGGAAAC GGCCAAAAAA GCGTGGAAGA CCACGAACTA TTCCTCGAGA   60

AAATATA   67

(2) INFORMATION FOR SEQ ID NO: 34:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 111 base pairs

            (B) TYPE: nucleic acid

            (C) STRANDEDNESS: double

            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGATATTCTG GATCTGATAG TGATTCCATC TCAGAAAGAA AACGACCAAA AAAACGTGGA   60

CGACCACGAA CTATTCCCCG TGAAAACATT AAAGGATTTA GTGATGCAGA G   111

(2) INFORMATION FOR SEQ ID NO: 35:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 67 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTCCATCTCA GAAAGAAAAC GACCAAGAAA ACGTGGACGA CCACGAACTA TTCCTCGTGA   60

AAATATT   67

(2) INFORMATION FOR SEQ ID NO: 36:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 111 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GATCTGATAG TGACTCCATC TCAGAAAGAA AACGACCAAG AAAACGTGGA CGACCACGAA   60

CTATCCCTCG GGAGAATATT AAAGGATTTA GCGATGCAGA GATTAGGCGG T   111

(2) INFORMATION FOR SEQ ID NO: 37:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 24 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc = "Synthetic DNA Primer"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATATTCTGGA TCTGATAGTG AYTC   24

(2) INFORMATION FOR SEQ ID NO: 38:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 23 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc = "Synthetic DNA Primer"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AGATATTCCG GATCTGATAG TGA   23

(2) INFORMATION FOR SEQ ID NO: 39:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 20 base pairs

            (B) TYPE: nucleic acid

            (C) STRANDEDNESS: single

            (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

            (A) DESCRIPTION: /desc = "Synthetic DNA Primer"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TTTCCTAAAT CGCTACGTCT   20